

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: FIDDES, J.C.
ABRAHAM, J.D.
- (ii) TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH
FACTOR ANALOG
- (iii) NUMBER OF SEQUENCES: 69
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lehnhardt, Susan K
(B) REGISTRATION NUMBER: 33,943
(C) REFERENCE/DOCKET NUMBER: 21900-20089.10
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1969 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

F06070 0340560

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 970...1434
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTCATGCC	TCTTTCTCTC	CTTTTGTGTTG	TAGACGACTT	CAGCCTCTGT	CCTTTAATTT	60
TAAAGTTTAT	GCCCCACTTG	TACCCCTCGT	CTTTTGGTGA	TTTAGAGATT	TTCAAAGCCT	120
GCTCTGACAC	AGACTCTTCC	TTGGATTGCA	ACTTCTCTAC	TTTGGGGTGG	AAACGGCTTC	180
TCCGTTTTGA	AACGCTAGCG	GGGAAAAAAT	GGGGGAGAAA	GTTGAGTTTA	AACTTTTAAA	240
AGTTGAGTCA	CGGCTGGTTG	CGCACGAAAA	GCCCCGCGAGT	GTGGAGAAAG	CCTAAACGTG	300
GTTTGGGTGG	TGCGGGGGTT	GGGCGGGGGT	GACTTTTGGG	GGATAAGGGG	CGGTGGAGCC	360
CAGGGAATGC	CAAAGCCCTG	CCGCGGCCCTC	CGACGCGCGC	CCCCCGCCCC	TCGCCTCTCC	420
CCCGCCCCCG	ACTGAGGCCG	GGCTCCCCGC	CGGACTGATG	TCGCGCGCTT	GCGTGTTGTG	480
GCCGAAGCCG	CCGAACCTCAG	AGGCCGGCCC	CAGAAAACCC	GAGCGAGTAG	GGGGCGGCGC	540
GCAGGAGGGA	GGAGAACTGG	GGGCGCGGGA	GGCTGGTGGG	TGTGGGGGGT	GGAGATGTAG	600
AAGATGTGAC	GCCGCGGCC	GGCGGGTGCC	AGATTAGCGG	ACGGCTGCCC	GCGGTTGCAA	660
CGGGATCCCG	GGCGCTGCAG	CTTGGGAGGC	GGCTCTCCCC	AGGCGGCGTC	CGCGGAGACA	720
CCCATCTGTG	AACCCAGGT	CCCGGGCCGC	CGGCTCGCCG	CGCACCAGGG	GCCGGCGGAC	780
AGAAGAGCGG	CCGAGCGGCT	CGAGGCTGGG	GGACCGCGGG	CGCGGCCGCG	CGCTGCCGGG	840
CGGGAGGCTG	GGGGGCCGGG	GCCGGGGCCG	TGCCCCGAGC	GGGTCGGAGG	CCGGGGCCGG	900
GGCCGGGGGA	CGGCGGCTCC	CCGCGCGGCT	CCAGCGGCTC	GGGGATCCCG	GCCGGGCCCC	960
GCAGGGACC	ATG GCA GCC	GGG AGC ATC	ACC ACG CTG	CCC GCC TTG	CCC GAG	1011
	Met Ala Ala	Gly Ser Ile	Thr Thr Leu	Pro Ala Leu	Pro Glu	
	1	5	10			
GAT GGC GGC	AGC GGC GCC	TTC CCG CCC	GGC CAC TTC	AAG GAC CCC	AAG	1059
Asp Gly Gly	Ser Gly Ala	Phe Pro Pro	Gly His Phe	Lys Asp Pro	Lys	
15	20		25		30	
CGG CTG TAC	TGC AAA AAC	GGG GGC TTC	TTC CTG CGC	ATC CAC CCC	GAC	1107
Arg Leu Tyr	Cys Lys Asn	Gly Gly Phe	Phe Leu Arg	Ile His Pro	Asp	
	35		40		45	
GGC CGA GTT	GAC GGG GTC	CGG GAG AAG	AGC GAC CCT	CAC ATC AAG	CTA	1155
Gly Arg Val	Asp Gly Val	Arg Glu Lys	Ser Asp Pro	His Ile Lys	Leu	
	50		55		60	
CAA CTT CAA	GCA GAA GAG	AGA GGA GTT	GTG TCT ATC	AAA GGA GTG	TGT	1203
Gln Leu Gln	Ala Glu Glu	Arg Gly Val	Val Ser Ile	Lys Gly Val	Cys	
	65		70		75	
GCT AAC CGT	TAC CTG GCT	ATG AAG GAA	GAT GGA AGA	TTA CTG GCT	TCT	1251
Ala Asn Arg	Tyr Leu Ala	Met Lys Glu	Asp Gly Arg	Leu Leu Ala	Ser	
	80		85		90	
AAA TGT GTT	ACG GAT GAG	TGT TTC TTT	TTT GAA CGA	TTG GAA TCT	AAT	1299
Lys Cys Val	Thr Asp Glu	Cys Phe Phe	Phe Glu Arg	Leu Glu Ser	Asn	
	95		100		105	110
AAC TAC AAT	ACT TAC CGG	TCA AGG AAA	TAC ACC AGT	TGG TAT GTG	GCA	1347
Asn Tyr Asn	Thr Tyr Arg	Ser Arg Lys	Tyr Thr Ser	Trp Tyr Val	Ala	
	115		120		125	

CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446
Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

Met	Ala	Ala	Gly	Ser	Ile	Thr	Thr	Leu	Pro	Ala	Leu	Pro	Glu	Asp	Gly	
1				5					10					15		
Gly	Ser	Gly	Ala	Phe	Pro	Pro	Gly	His	Phe	Lys	Asp	Pro	Lys	Arg	Leu	
			20					25						30		
Tyr	Cys	Lys	Asn	Gly	Gly	Phe	Phe	Leu	Arg	Ile	His	Pro	Asp	Gly	Arg	
		35					40					45				
Val	Asp	Gly	Val	Arg	Glu	Lys	Ser	Asp	Pro	His	Ile	Lys	Leu	Gln	Leu	
	50					55					60					
Gln	Ala	Glu	Glu	Arg	Gly	Val	Val	Ser	Ile	Lys	Gly	Val	Cys	Ala	Asn	
65					70					75					80	
Arg	Tyr	Leu	Ala	Met	Lys	Glu	Asp	Gly	Arg	Leu	Leu	Ala	Ser	Lys	Cys	
				85				90						95		
Val	Thr	Asp	Glu	Cys	Phe	Phe	Phe	Glu	Arg	Leu	Glu	Ser	Asn	Asn	Tyr	
			100					105					110			
Asn	Thr	Tyr	Arg	Ser	Arg	Lys	Tyr	Thr	Ser	Trp	Tyr	Val	Ala	Leu	Lys	
		115					120					125				
Arg	Thr	Gly	Gln	Tyr	Lys	Leu	Gly	Ser	Lys	Thr	Gly	Pro	Gly	Gln	Lys	
	130					135					140					
Ala	Ile	Leu	Phe	Leu	Pro	Met	Ser	Ala	Lys	Ser						
145					150					155						

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 638 base pairs
(B) TYPE: nucleic acid

TGCATTTTGT	GCCTTTGCTG	GAAGAACCGA	CTACAGGTTT	GTTCAATTTC	TTACAGTCTT	60
GAAAGCGCCA	CAAGCAGCAG	CTGCTGAGCC	ATG GCT GAA GGG GAA ATC ACC ACC	114		
			Met Ala Glu Gly Glu Ile Thr Thr			
			1 5			
TTC ACA GCC CTG ACC GAG AAG TTT AAT CTG CCT CCA GGG AAT TAC AAG	162					
Phe Thr Ala Leu Thr Glu Lys Phe Asn Leu Pro Pro Gly Asn Tyr Lys						
10 15 20						
AAG CCC AAA CTC CTC TAC TGT AGC AAC GGG GGC CAC TTC CTG AGG ATC	210					
Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile						
25 30 35 40						
CTT CCG GAT GGC ACA GTG GAT GGG ACA AGG GAC AGG AGC GAC CAG CAC	258					
Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His						
45 50 55						
ATT CAG CTG CAG CTC AGT GCG GAA AGC GTG GGG GAG GTG TAT ATA AAG	306					
Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys						
60 65 70						
AGT ACC GAG ACT GGC CAG TAC TTG GCC ATG GAC ACC GAC GGG CTT TTA	354					
Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu						
75 80 85						
TAC GGC TCA CAG ACA CCA AAT GAG GAA TGT TTG TTC CTG GAA AGG CTG	402					
Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu						
90 95 100						
GAG GAG AAC CAT TAC AAC ACC TAT ATA TCC AAG AAG CAT GCA GAG AAG	450					
Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys						
105 110 115 120						
AAT TGG TTT GTT GGC CTC AAG AAG AAT GGG AGC TGC AAA CGC GGT CCT	498					
Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro						
125 130 135						
CGG ACT CAC TAT GGC CAG AAA GCA ATC TTG TTT CTC CCC CTG CCA GTC	546					
Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val						
140 145 150						
TCT TCT GAT TAAAGAGATC TGTTCTGGGT GTTGACCACT CCAGAGAAGT TTCGAGGGG	604					
Ser Ser Asp						
155						

TCCTCACCTG GTTGACCCAA AAATGTTCCC TTGA

638

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Glu	Gly	Glu	Ile	Thr	Thr	Phe	Thr	Ala	Leu	Thr	Glu	Lys	Phe
1				5					10					15	
Asn	Leu	Pro	Pro	Gly	Asn	Tyr	Lys	Lys	Pro	Lys	Leu	Leu	Tyr	Cys	Ser
			20					25					30		
Asn	Gly	Gly	His	Phe	Leu	Arg	Ile	Leu	Pro	Asp	Gly	Thr	Val	Asp	Gly
		35					40					45			
Thr	Arg	Asp	Arg	Ser	Asp	Gln	His	Ile	Gln	Leu	Gln	Leu	Ser	Ala	Glu
	50					55					60				
Ser	Val	Gly	Glu	Val	Tyr	Ile	Lys	Ser	Thr	Glu	Thr	Gly	Gln	Tyr	Leu
65					70				75					80	
Ala	Met	Asp	Thr	Asp	Gly	Leu	Leu	Tyr	Gly	Ser	Gln	Thr	Pro	Asn	Glu
			85						90					95	
Glu	Cys	Leu	Phe	Leu	Glu	Arg	Leu	Glu	Glu	Asn	His	Tyr	Asn	Thr	Tyr
		100					105					110			
Ile	Ser	Lys	Lys	His	Ala	Glu	Lys	Asn	Trp	Phe	Val	Gly	Leu	Lys	Lys
	115						120					125			
Asn	Gly	Ser	Cys	Lys	Arg	Gly	Pro	Arg	Thr	His	Tyr	Gly	Gln	Lys	Ala
	130					135					140				
Ile	Leu	Phe	Leu	Pro	Leu	Pro	Val	Ser	Ser	Asp					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGAATTCAAA	TATTCTGAAA	TGAGCTGTTG	ACAATTAATC	ATCGAACTAG	TTAACTAGTA	60
CGCAAGTTCA	CGTAAAAGG	GTATCACATA	TGGTACCTGC	AGA		103

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

TCTGCAGGTA CCATATGTGA TACCCTTTTT ACGTGAACTT GCGTACTAGT TAACTAGTTC 60
GATGATTAAT TGTCAACAGC TCATTTTCTA ATATTTGAAT TCT 103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

GAAATACACC AGTTGG 16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ACTTGGATCC AAAACAG 17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

TTTACATGA AGCTTTATAT TTCAG 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGCTTCATAT GGCTGCTGGT TCTATCACTA CC

32

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGCCAGCTC TGCCAGAAGA CGGTGGTT

28

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGGTGCCTT CCCACCAGGT CACTTCAA

28

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGACCCAAAA CGTCTGTACT GCAAAAAC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGTGGTTTCT TCCTGCGCA

19

L06070-0340560

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAGAACCAGC AGCCATATGA

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCTTCTGGCA GAGCTGGCAG GGTAGTGA

--28--

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACCTGGTGGG AAGGCACCAG AACCACCG

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGTACAGACG TTTTGGGTCT TTGAAGTG

28

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCTTGCGCA GGAAGAAACC ACCGTTTTTG C

31

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTTCATAT GGCTGCTGGT TCTATCACTA CCCTGCCAGC TCTGCCAGAA GACGGTGGTT	60
CTGGTGCCCTT CCCACCAGGT CACTTCAAAG ACCCAAACG TCTGTACTGC AAAAACGGTG	120
GTTTCTTCCT GCGCA	135

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCTTGCGCA GGAAGAAACC ACCGTTTTTG CAGTACAGAC GTTTTGGGTC TTTGAAGTGA	60
CCTGGTGGGA AGGCACCAGA ACCACCGTCT TCTGGCAGAG CTGGCAGGGT AGTGATAGAA	120
CCAGCAGCCA TATGA	135

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGTCTGTAC TCCAAAACG GTG

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TACAGACGAG TCTTTCTTTT TTG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCTGTACTG CTCAAACGGT GGTT

24

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTCTTCCTG CTCATCCACC CCG

23

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CATCCACCCC GCCGGCCGAG TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCCCGACGGC CTAGTGGACG GGG

23

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(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACCCCGACGG CGCAGTGGAC GGGG

24

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGCCGGAGT GGCCGGGGTC CGCG

24

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GAGTGGACGG GAAACGCGAG AAGAG

25

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGACGGGGTC CTCGAGAAGA GCG

23

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid

1060200340650

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTCCGCGAG ATGAGCGACC CAC

23

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTCCGCGAG ATAAGCGACC CACA

24

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGAGAAGAGC GCCCCACACA TCA

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAGCGACCCA AACATCAAAC TAC

23

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAAGATGGA ACTTTACTAG CTTC

24

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGTGTTACA GCAGAGTGTT TCT

23

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTTACAGACG CCTGTTTCTT TTTTG

25

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTGTTACAGA CAGTTGTTTC TTTT

25

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTTTCTTTTT TTCACGATTG GAGT

24

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(D) TOPOLOGY: linear

23

(D) TOPOLOGY: linear

24

(D) TOPOLOGY: linear

25

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(D) TOPOLOGY: linear
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23

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAATACTTAC ACTTCAAGGA AATA

24

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAATACTTAC CTGTCAAGGA AAT

23

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ACCGGTCAAG GTCTTACACC AGTTG

25

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGTGGTTTCT TCCACCCCGA CGGC

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

105020-0340600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCCGACGGCC GAGTCCGCGA GAAG

24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCACACATCA AACAAGCAGA AGAG

24

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCAAACCGTT ACAAAGAAGA TGGA

24

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TGTTTCTTTT TTGAGTCTAA TAAC

24

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAGTCTAATA ACTACCGGTC AAGG

24

T05020"094050

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AGGTCACTTC ATGGACCCAA AACG

24

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TCAAAGACCC AGCACGTCTG TACT

24

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAGACCCAAA ATCTCTGTAC TGCA

24

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTCACTTCAA AAAGCCAAAA CGTCT

25

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid

T05020-034050

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGCACTGAAA ACTACTGGGC AGT

23

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGGGCAGTA TTCTCTTGA TCCAA

25

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AACTTGGATC CTCTACAGGA CCTGG

25

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TTGGGTCTTT GAAGTGCATA TGTGGGAAGG CACCAG

36